in the name of **GOD**

Target Scan

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2016/12/31

- **Introduction**
  General Information about miRNAs
  & Biogenesis

- **Target Prediction of miRNAs**
  Features/Parameters for miRNA target prediction

- **Methodology**
  Target prediction - Gathering and handling data

- **Results**
- **References**

Introduction

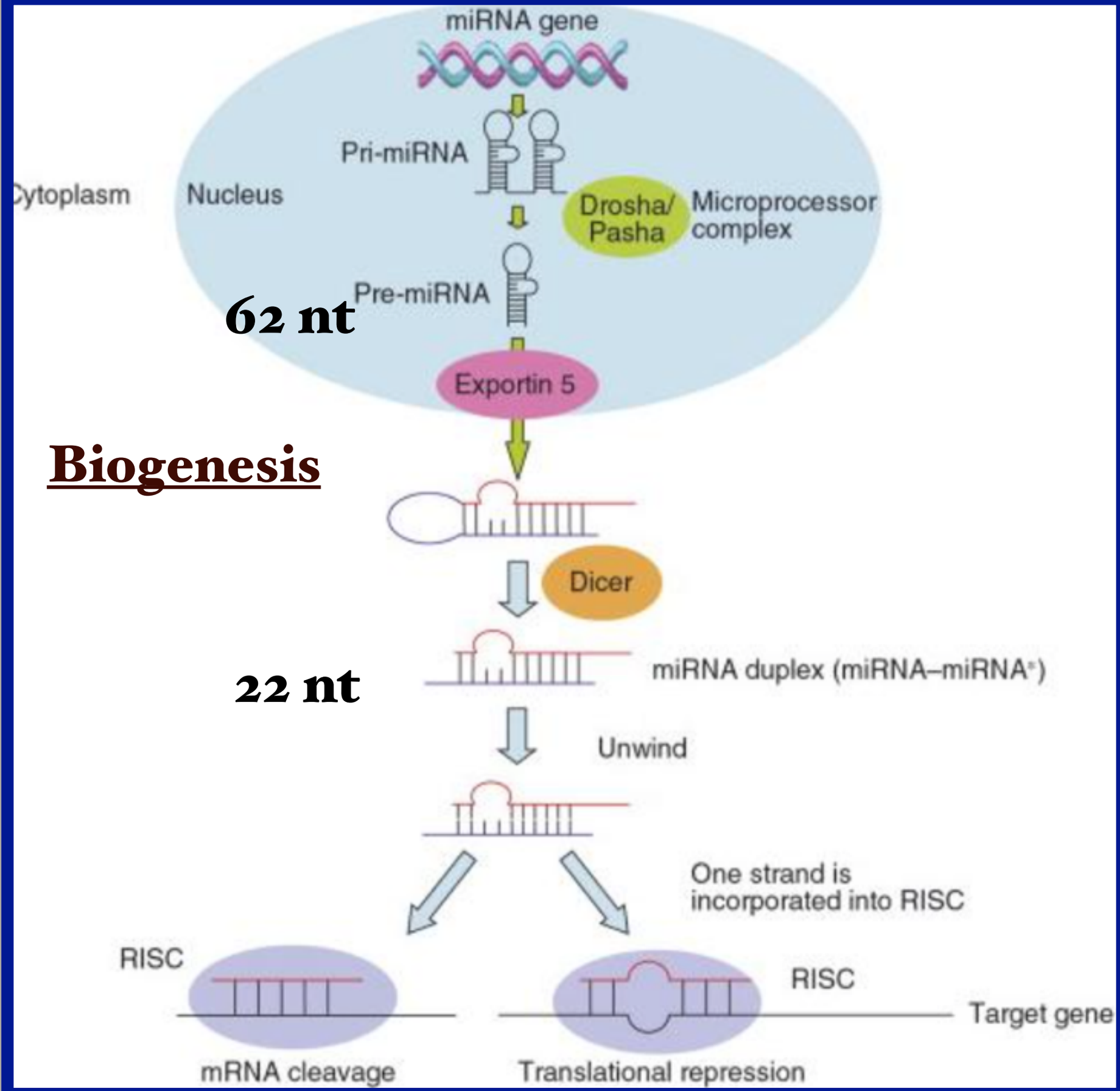
General Information about miRNAs

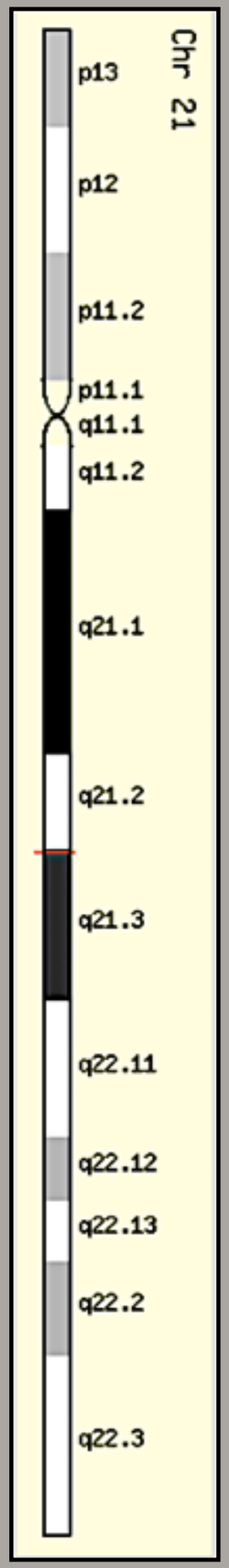
- Micro RNAs (miRNAs) are short (**19-24**) nucleotide(nt)
- binding to **3' untranslated regions (UTRs)**
- up to **60%** of all mammalian genes
- first miRNA was discovered in 1993 **(lin-4)**(1)
- **24521** miRNAs in **206 species** are known(2)

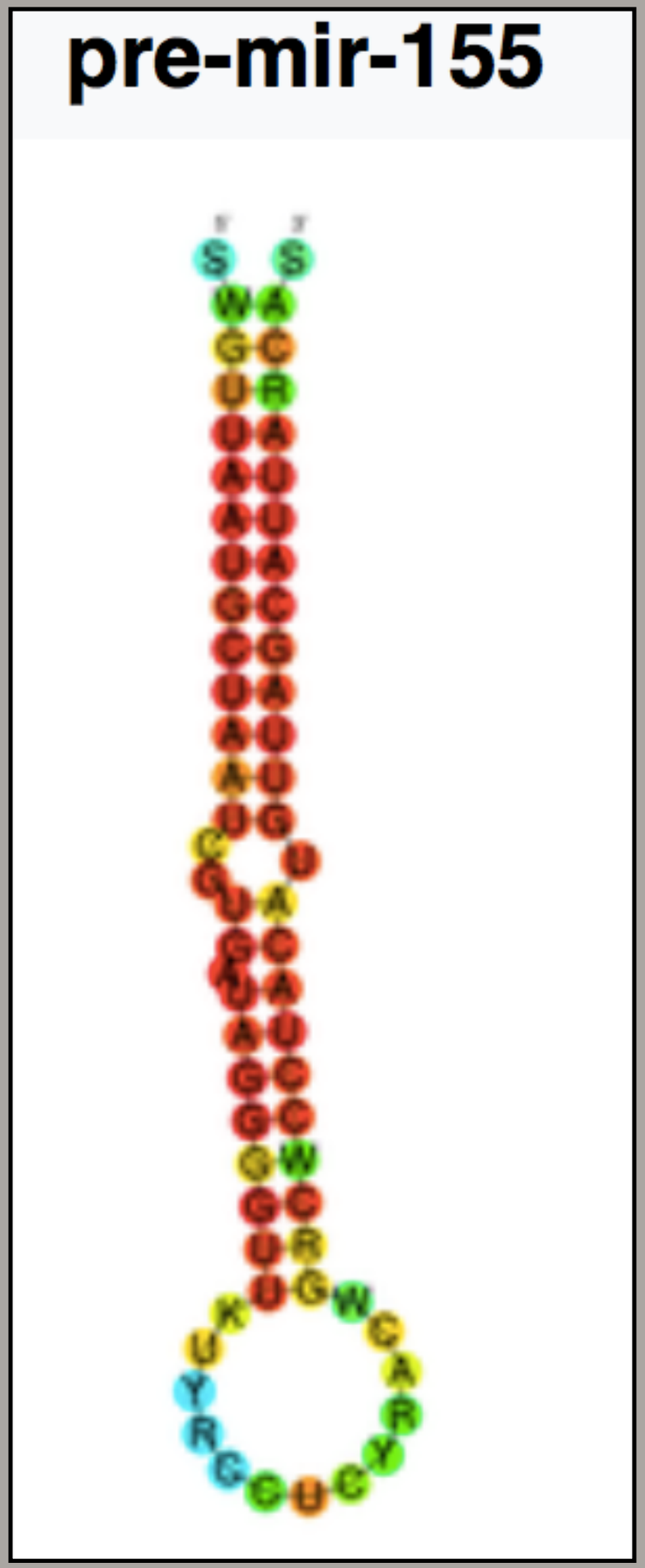
Biogenesis

- **RNA Polymerase II (RNA Pol II)**
- **Primary miRNAs**
- **Precursor miRNA (pre-miRNA)**
- **RNA-induced silencing complex (RISC)**[3]

Biogenesis


miRNA gene
Pri-miRNA
Cytoplasm
Nucleus
Drosha/
Pasha
Microprocessor
complex
62 nt
Pre-miRNA
Exportin 5
Dicer
22 nt
miRNA duplex (miRNA–miRNA*)
Unwind
One strand is
incorporated into RISC
RISC
RISC
Target gene
mRNA cleavage
Translational repression





MiR-155

BIC (B-cell Integration Cluster)

List of **target prediction** softwares/databases

Name	URL	Availability
TargetScan	http://targetscan.org/	Online
RNA22	http://cbcsrv.watson.ibm.com/rna22.html	Online
miRWalk	http://miRWalk.org	online
DIANA-microT	http://diana.cslab.ece.ntua.gr/microT/	Online
miRanda	http://www.microrna.org/microrna/home.do	Download
PicTar	http://pictar.mdc-berlin.de	Online
MicroTar	http://tiger.dbs.nus.edu.sg/microtar/	Download

Summary of the miRNA target prediction tools

TargetScan

- **Predicting microRNA target sites**
- Human, dog, chimpanzee, rat, mouse, chicken, rhesus, cow, frog , opossum, worm and fly
- Conserved target sites
- **Seed pairing**
- **Thermodynamic stability** of the binding site
- Context score(4)

Target Prediction of miRNAs

- **Seed site**
- **Site location**
- **Conservation**
- **Site accessibility**
- **Multiple sites in single target**
- **Expression profile** (4)

Features Parameters for miRNA target prediction

Seed site is the most important feature for target recognition(1)
(positions 2–7 from the 5′ end of miRNA)

8mer sites

An exact match to positions **2-8** of the mature miRNA (seed + position 8) followed by an ‘A'

7mer sites

7mer-m8

(the seed + position 8)

7mer-A1

2-7 of the mature miRNA (seed) followed by an ‘A'

6mer sites

2-7 of the mature miRNA (seed)
All 6-mer sites are classified as **poorly conserved (4, 5)**

Seed site

6mer site – Seed match

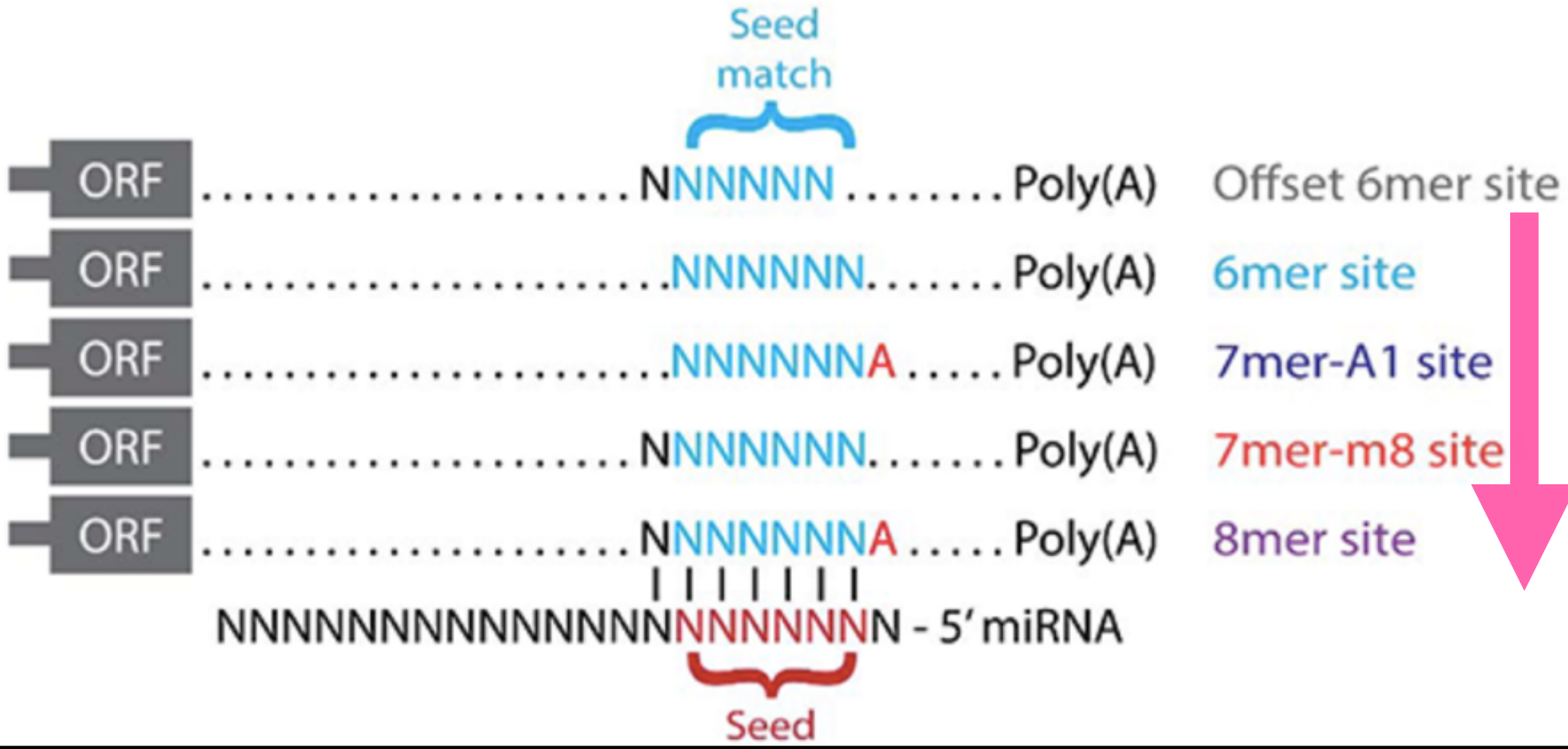
7mer-A1 site – Seed match + A at position 1

7mer-m8 site – Seed match + match at position 8

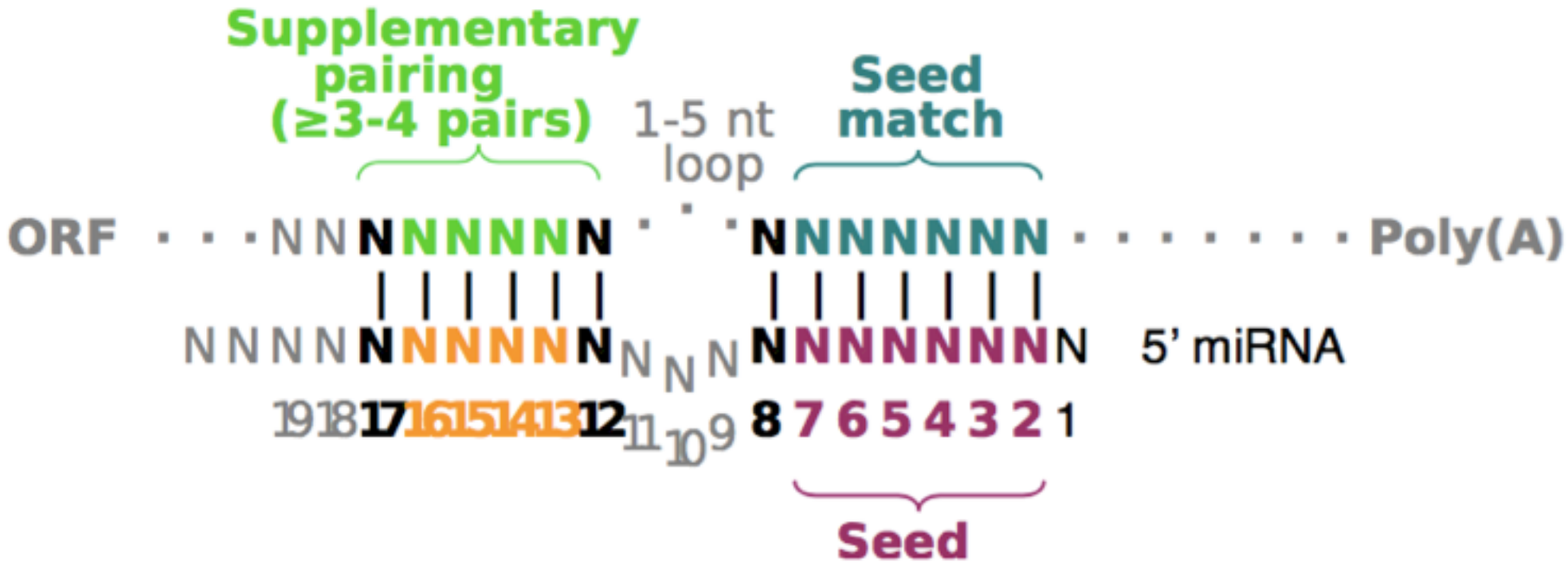
8mer site – Seed match + A1 and m8

Canonical site types

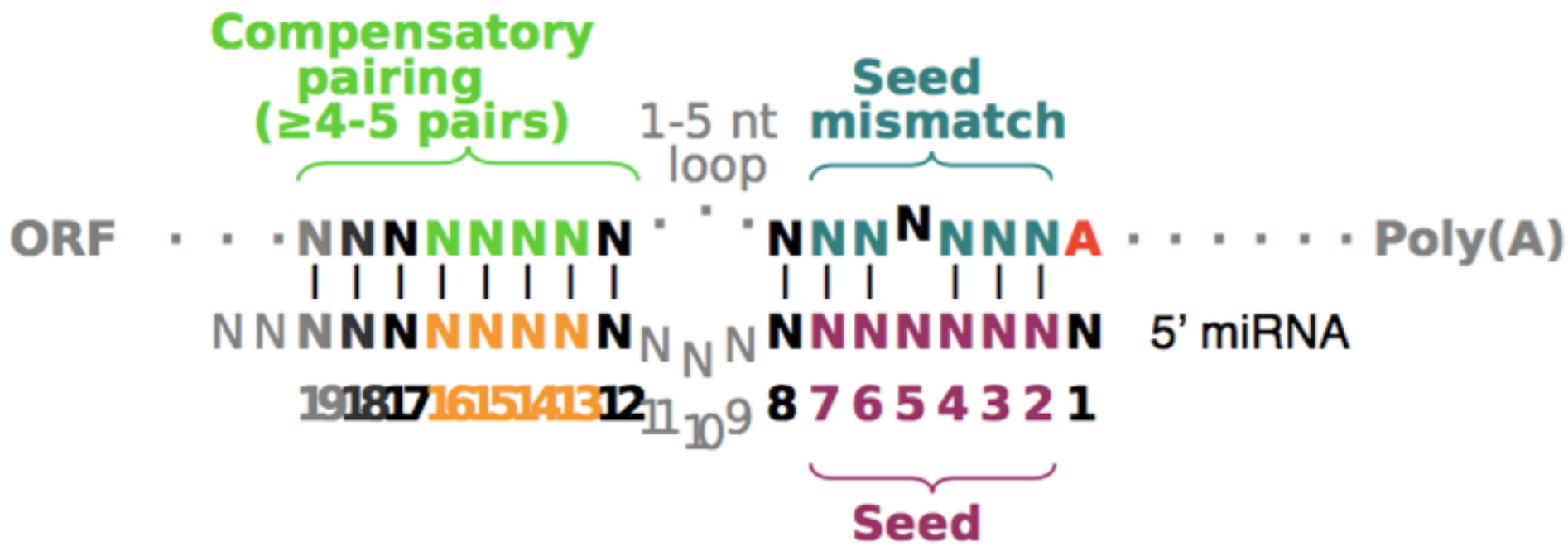
stringent seed



3'supplementary site – Seed match with supplementary pairing



3' compensatory site – Seed mismatch with compensatory pairing



Site location

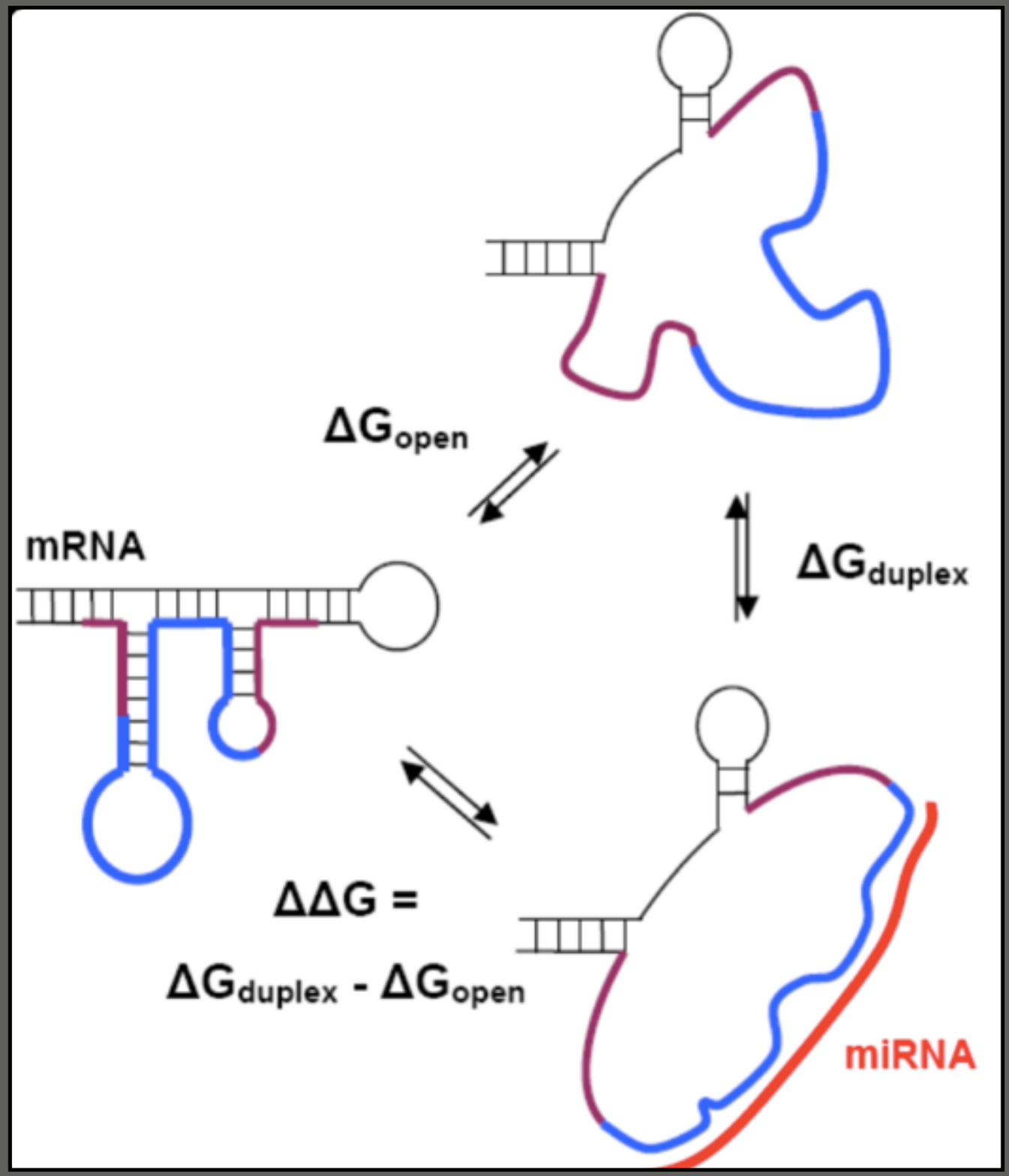
Conservation: Targets and miRNAs are conserved among related species

* Most target sites of miRNAs are located in **3UTRs** of target genes
* **CDS(coding DNA sequence)** and **5UTR** is more difficult for **RISC**
* MiRNAs that have the same seed site belong to the same miRNA family (4).

Accessibility

* secondary structure of mRNA
Target sites have to be accessible meaning that they have to be opened

* AU content is preferential meaning that it is easy to access mRNA and bind to it
due to less hydrogen bond between A and U



MiR-155 Target Prediction and Validation in Nasopharyngeal Carcinoma

Multiple sites in single target (4)

Expression profile miRNA

Single miRNA is capable of regulating many genes(4)

Pct

Context score(6)

Pct

Probability of conserved targeting

has been calculated for
all highly conserved miRNA (4)

$$1 - (\quad (1 - P_{CT})_{site1} \quad x \quad (1 - P_{CT})_{site2} \quad x \quad (1 - P_{CT})_{site3} \ldots \quad)$$

context score

The context++ score (CS) for a specific site

- **site type**
- **supplementary pairing**
- **local AU**
- **minimum distance**
- **3' UTR length**
- **SA**(structural accessibility)
- **ORF(open reading frames) length**
- **ORF 8mer count**
- **TA (target site abundance)**
- **SPS (seed-pairing stability)**
- **$P_{CT\ (7)}$**

TargetScanHuman

Prediction of microRNA targets

Release 7.1: June 2016

Agarwal *et al.*, 2015

Search for predicted microRNA targets in mammals

[Go to TargetScanMouse]
[Go to TargetScanWorm]
[Go to TargetScanFly]
[Go to TargetScanFish]

1. Select a species: Human

AND

2. Enter a human gene symbol (e.g. "Hmga2") or an Ensembl gene (ENSG00000149948) or transcript (ENST00000403681) ID: ENSG00000185338

AND/OR

3. Do one of the following:

- Select a broadly conserved* microRNA family: Broadly conserved microRNA families
- Select a conserved* microRNA family: Conserved microRNA families
- Select a poorly conserved but confidently annotated microRNA family: Poorly conserved microRNA families
- Select another miRBase annotation: Other miRBase annotations

Note that most of these families are star miRNAs or RNA fragments misannotated as miRNAs.

- Enter a microRNA name (e.g. "miR-9-5p": miR-155

TargetScanHuman
Prediction of microRNA targets

Release 7.1: June 2016

Agarwal *et al.*, 2015

hsa-miR-155 matches multiple families in our miRNA database:

miR-155-5p	broadly conserved
miR-155-3p	very poorly conserved

You may wish to consult our list of miRNAs and miRNA families.

TargetScanHuman

Prediction of microRNA targets

Release 7.1: June 2016 Agarwal *et al.*, 2015

Human | miR-155-5p

552 transcripts with conserved sites, containing a total of **592** conserved sites and **239** poorly conserved sites.

Genes with only poorly conserved sites are not shown. [View top predicted targets, irrespective of site conservation]

Table sorted by cumulative weighted context++ score [Sort table by aggregate P_{CT}]

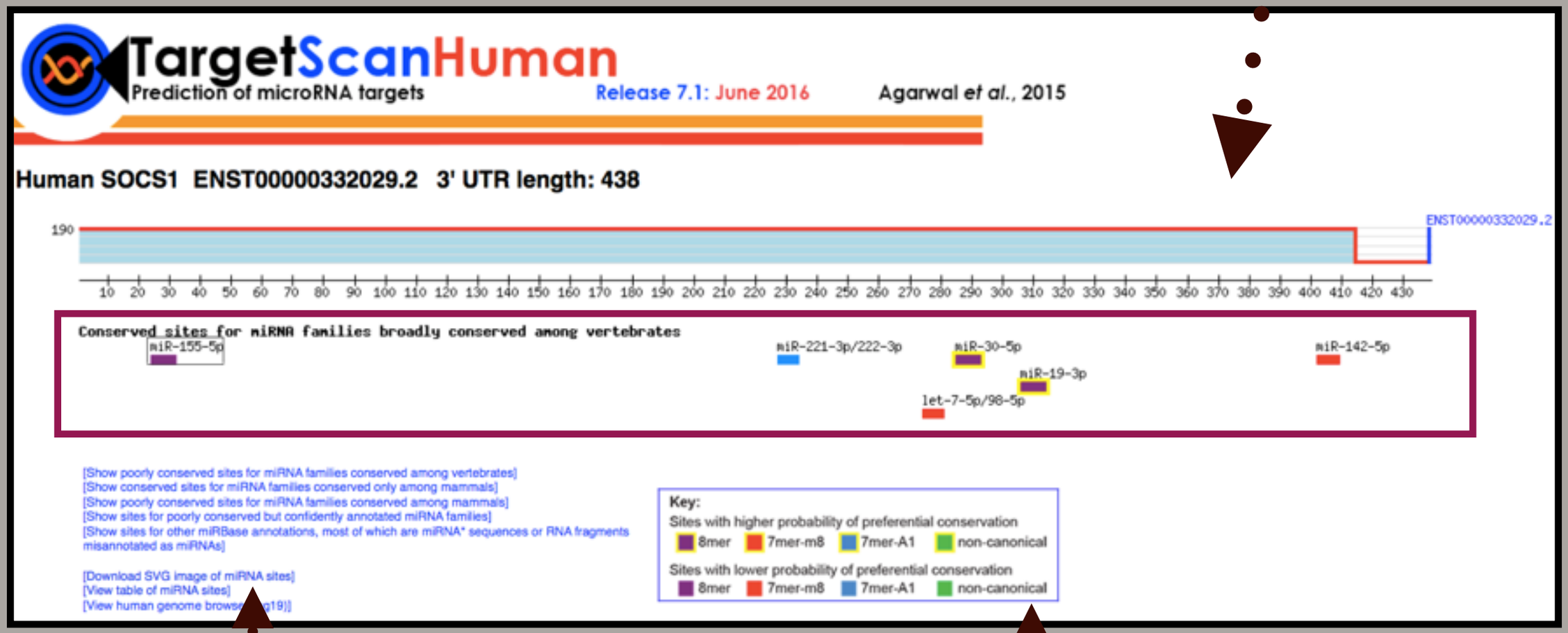
The table shows at most one transcript per gene, selected for being the most prevalent, based on 3P-seq tags (or the one with the longest 3' UTR, in case of a tie). [Download table]

Target gene	Representative transcript	Gene name	Number of 3P-seq tags supporting UTR + 5	Link to sites in UTRs	Conserved sites				Poorly conserved sites				6mer sites	Representative miRNA	Cumulative weighted context++ score	Total context++ score
					total	8mer	7mer-m8	7mer-A1	total	8mer	7mer-m8	7mer-A1				
ZNF385D	ENST00000281523.2	zinc finger protein 385D	5	Sites in UTR	1	0	0	1	4	1	1	2	1	hsa-miR-155-5p	-0.80	-0.80
TMPRSS11BNL	ENST00000432593.3	TMPRSS11B N-terminal like	5	Sites in UTR	1	1	0	0	2	1	1	0	0	hsa-miR-155-5p	-0.68	-0.68
VAV3	ENST00000370056.4	vav 3 guanine nucleotide exchange factor	1128	Sites in UTR	1	1	0	0	1	1	0	0	0	hsa-miR-155-5p	-0.64	-0.64
ACTA1	ENST00000366684.3	actin, alpha 1, skeletal muscle	14	Sites in UTR	1	1	0	0	0	0	0	0	0	hsa-miR-155-5p	-0.59	-0.59
ARID2	ENST00000457135.1	AT rich interactive domain 2 (ARID, RFX-like)	891	Sites in UTR	2	1	1	0	0	0	0	0	1	hsa-miR-155-5p	-0.58	-0.58
H3F3A	ENST00000366813.1	H3 histone, family 3A	15	Sites in UTR	1	1	0	0	0	0	0	0	0	hsa-miR-155-5p	-0.58	-0.58
ETS1	ENST00000345075.4	v-ets avian erythroblastosis virus E26 oncogene homolog 1	1423	Sites in UTR	2	2	0	0	0	0	0	0	1	hsa-miR-155-5p	-0.57	-0.60
ZNF652	ENST00000362063.2	zinc finger protein 652	33	Sites in UTR	2	1	1	0	2	0	1	1	3	hsa-miR-155-5p	-0.57	-0.70
VMA21	ENST00000330374.6	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae)	2162	Sites in UTR	1	1	0	0	0	0	0	0	0	hsa-miR-155-5p	-0.54	-0.54
ACTL7A	ENST00000333999.3	actin-like 7A	5	Sites in UTR	1	1	0	0	0	0	0	0	0	hsa-miR-155-5p	-0.53	-0.53
TM6SF1	ENST00000379390.6	transmembrane 6 superfamily member 1	211	Sites in UTR	1	1	0	0	0	0	0	0	0	hsa-miR-155-5p	-0.53	-0.53
CEBPB	ENST00000303004.3	CCAAT/enhancer binding protein (C/EBP), beta	3178	Sites in UTR	1	1	0	0	0	0	0	0	0	hsa-miR-155-5p	-0.52	-0.56
FOS	ENST00000303562.4	FBJ murine osteosarcoma viral oncogene homolog	3716	Sites in UTR	1	1	0	0	0	0	0	0	2	hsa-miR-155-5p	-0.52	-0.55
WWC1	ENST00000265293.4	WW and C2 domain containing 1	43	Sites in UTR	1	1	0	0	0	0	0	0	0	hsa-miR-155-5p	-0.52	-0.52
TAOK1	ENST00000261716.3	TAO kinase 1	164	Sites in UTR	1	0	0	1	2	0	0	2	1	hsa-miR-155-5p	-0.51	-0.56
TMEM202	ENST00000341689.3	transmembrane protein 202	5	Sites in UTR	1	1	0	0	1	0	1	0	0	hsa-miR-155-5p	-0.50	-0.74
TSHZ3	ENST00000240587.4	teashirt zinc finger homeobox 3	81	Sites in UTR	3	1	0	2	0	0	0	0	0	hsa-miR-155-5p	-0.50	-0.62

SOCS1	ENST00000332029.2	suppressor of cytokine signaling 1	190	Sites in UTR
PDSS2	ENST00000369031.4	prenyl (decaprenyl) diphosphate synthase, subunit 2	42	Sites in UTR
FBXL17	ENST00000359660.5	F-box and leucine-rich repeat protein 17	182	Sites in UTR
XKR4	ENST00000327381.6	XK, Kell blood group complex subunit-related family, member 4	5	Sites in UTR
KDM5B	ENST00000367265.3	lysine (K)-specific demethylase 5B	187	Sites in UTR
UPP2	ENST00000605860.1	uridine phosphorylase 2	5	Sites in UTR
C5orf64	ENST00000505642.1	chromosome 5 open reading frame 64	5	Sites in UTR
CKAP5	ENST00000529230.1	cytoskeleton associated protein 5	2192	Sites in UTR
C7orf71	ENST00000409974.3	chromosome 7 open reading frame 71	5	Sites in UTR
HIVEP2	ENST00000367604.1	human immunodeficiency virus type I enhancer binding protein 2	137	Sites in UTR
FAM83D	ENST00000217429.4	family with sequence similarity 83, member D	600	Sites in UTR
MBTD1	ENST00000586178.1	mbt domain containing 1	113	Sites in UTR
ATXN1L	ENST00000427980.2	ataxin 1-like	12	Sites in UTR
SOCS5	ENST00000306503.5	suppressor of cytokine signaling 5	72	Sites in UTR
C8orf44-SGK3	ENST00000519289.1	C8orf44-SGK3 readthrough	56	Sites in UTR
METTL21A	ENST00000448823.2	methyltransferase like 21A	224	Sites in UTR
TMEM200C	ENST00000581347.2	transmembrane protein 200C	54	Sites in UTR
CSNK1G2	ENST00000255641.8	casein kinase 1, gamma 2	5	Sites in UTR
VEZF1	ENST00000584396.1	vascular endothelial zinc finger 1	209	Sites in UTR
TAB2	ENST00000367456.1	TGF-beta activated kinase 1/MAP3K7 binding protein 2	1129	Sites in UTR

Number of 3P-seq tags supporting UTR + 5	Link to sites in UTRs	Conserved sites				Poorly conserved sites				6mer sites	Representative miRNA	Cumulative weighted context++ score	Total context++ score	Aggregate P_{CT}
		total	8mer	7mer-m8	7mer-A1	total	8mer	7mer-m8	7mer-A1					
5	Sites in UTR	**1**	0	0	1	**4**	1	1	2	1	hsa-miR-155-5p	-0.80	-0.80	0.64
5	Sites in UTR	**1**	1	0	0	**2**	1	1	0	0	hsa-miR-155-5p	-0.68	-0.68	0.24
1128	Sites in UTR	**1**	1	0	0	**1**	1	0	0	0	hsa-miR-155-5p	-0.64	-0.64	< 0.1
14	Sites in UTR	**1**	1	0	0	**0**	0	0	0	0	hsa-miR-155-5p	-0.59	-0.59	0.42
891	Sites in UTR	**2**	1	1	0	**0**	0	0	0	1	hsa-miR-155-5p	-0.58	-0.58	0.71
15	Sites in UTR	**1**	1	0	0	**0**	0	0	0	0	hsa-miR-155-5p	-0.58	-0.58	0.34
1423	Sites in UTR	**2**	2	0	0	**0**	0	0	0	1	hsa-miR-155-5p	-0.57	-0.60	0.52
33	Sites in UTR	**2**	1	1	0	**2**	0	1	1	3	hsa-miR-155-5p	-0.57	-0.70	0.93
2162	Sites in UTR	**1**	1	0	0	**0**	0	0	0	0	hsa-miR-155-5p	-0.54	-0.54	< 0.1
5	Sites in UTR	**1**	1	0	0	**0**	0	0	0	0	hsa-miR-155-5p	-0.53	-0.53	< 0.1
211	Sites in UTR	**1**	1	0	0	**0**	0	0	0	0	hsa-miR-155-5p	-0.53	-0.53	N/A

لیست میرهای بسیار حفاظت شده برای این ژن و محل اتصال آنها



دانلود اطلاعات کل میر به صورت جدول

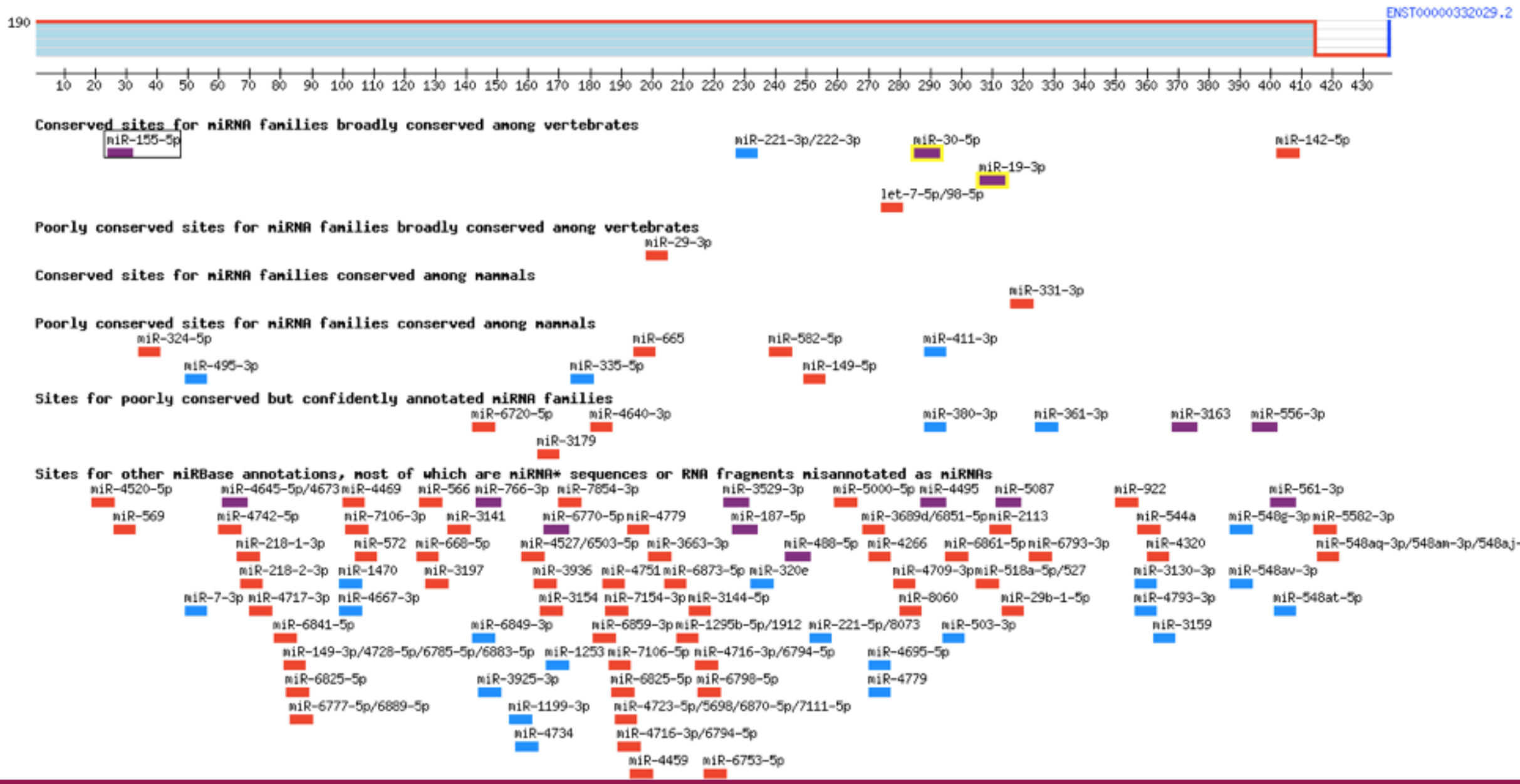
اطلاعات ناحیه seed مانند تعداد بازهای جفت شده

[Show poorly conserved sites for miRNA families conserved among vertebrates]
[Show conserved sites for miRNA families conserved only among mammals]
[Show poorly conserved sites for miRNA families conserved among mammals]
[Show sites for poorly conserved but confidently annotated miRNA families]
[Show sites for other miRBase annotations, most of which are miRNA* sequences or RNA fragments misannotated as miRNAs]

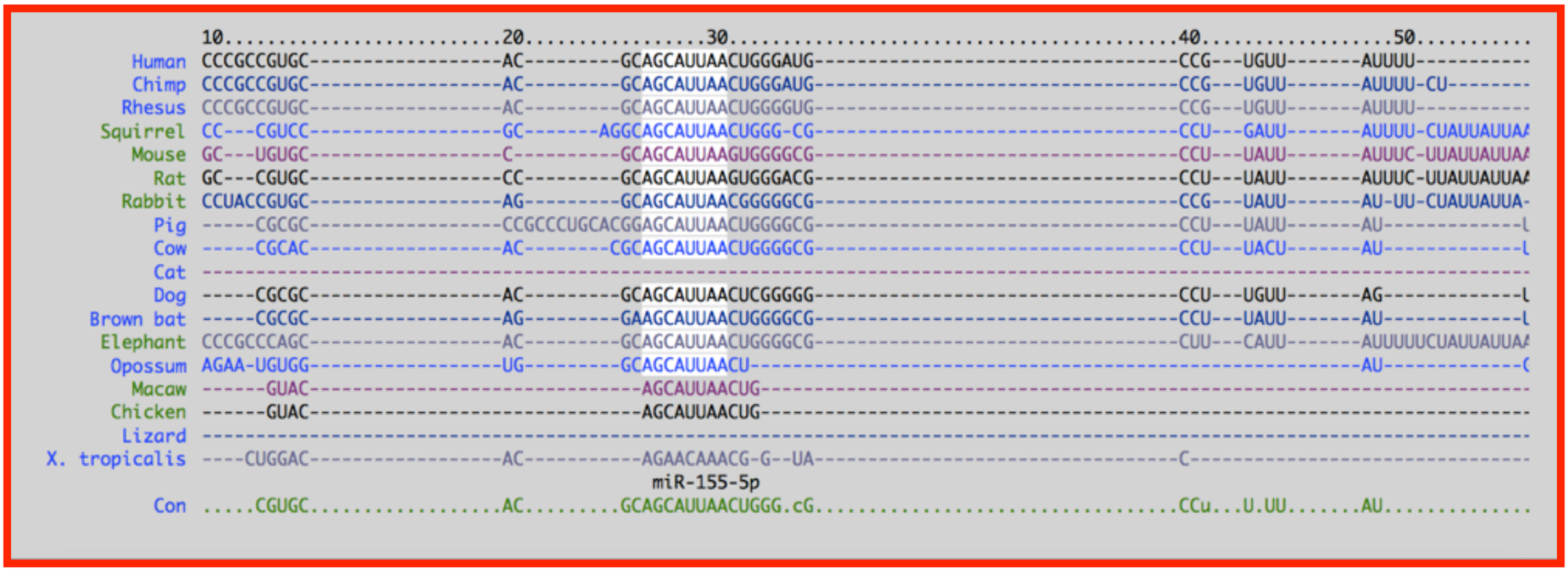
[Download SVG image of miRNA sites]
[View table of miRNA sites]
[View human genome browser (hg19)]

TargetScanHuman
Prediction of microRNA targets
Release 7.1: June 2016
Agarwal *et al.*, 2015

Human SOCS1 ENST00000332029.2 3' UTR length: 438



توالی این ژن در موجودات مختلف و جایگاه میر



لیست میرها و نحوه اتصال و امتیاز هر کدام

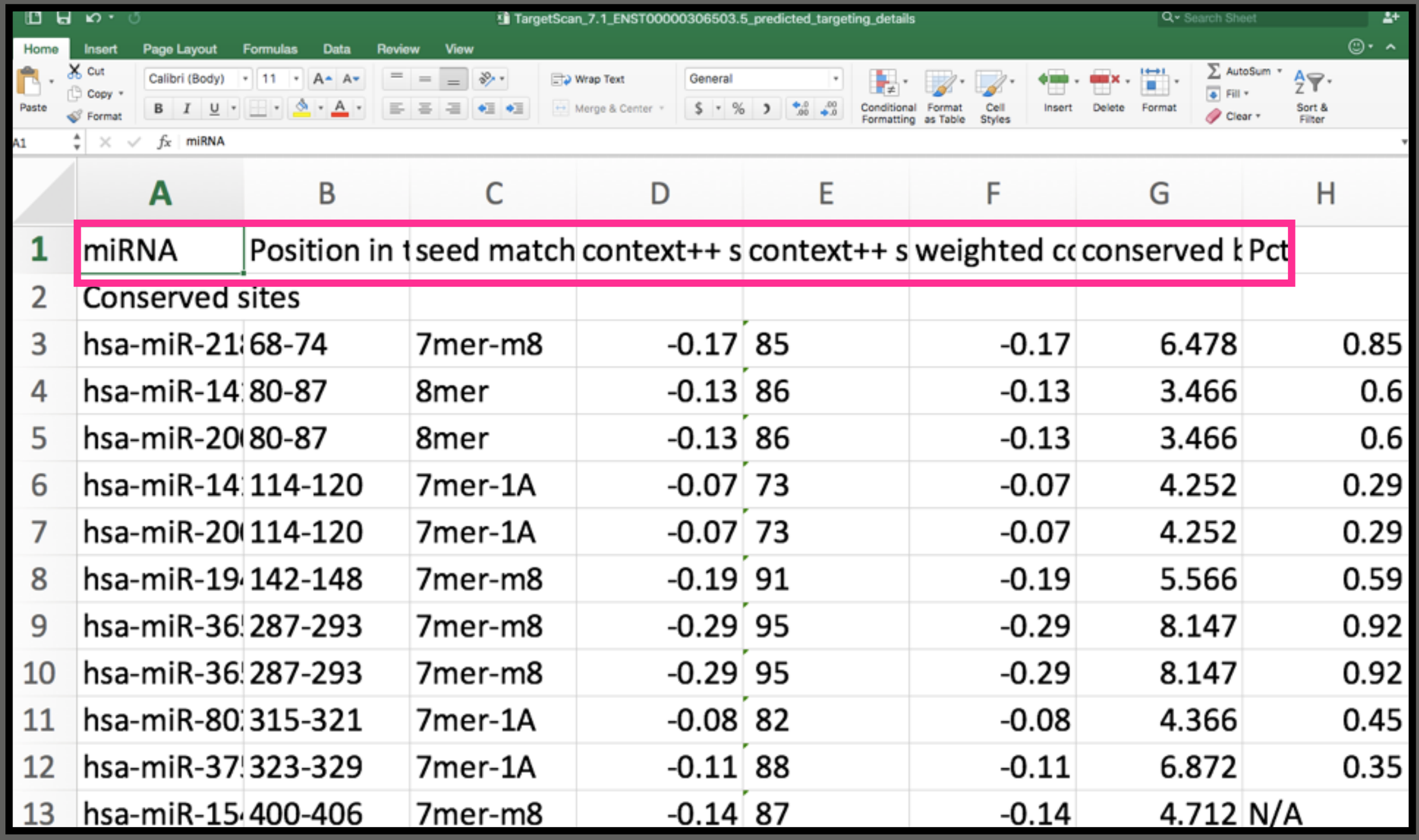
[Download table]

Conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 24-31 of SOCS1 3' UTR	5' ...GCCCGCCGUGCACGC--AGCAUUAA...	8mer	-0.33	97	-0.33	3.691	0.38
hsa-miR-155-5p	3' UGGGGAUAGUGCUAAUCGUAAUU						

TargetScan_7.1_ENST00000332029.2_predicted_targeting_details.txt
TargetScan_7.1_ENST00000332029.2_predicted_targeting_details.xlsx

miRNA	Position in the UTR	seed match		context++ score	context++ score percentile
Conserved sites					
hsa-miR-155-5p	24-31	8mer	-0.33	97	-0.33	3.691	0.38
hsa-miR-221-3p	227-233	7mer-1A	-0.19	85	-0.19	4.177	0.38
hsa-miR-222-3p	227-233	7mer-1A	-0.19	85	-0.19	4.177	0.38
hsa-let-7g-5p	274-280	7mer-m8	-0.42	96	-0.42	3.218	0.50
hsa-let-7a-5p	274-280	7mer-m8	-0.43	96	-0.43	3.218	0.50
hsa-let-7i-5p	274-280	7mer-m8	-0.43	96	-0.43	3.218	0.50
hsa-let-7d-5p	274-280	7mer-m8	-0.43	96	-0.43	3.218	0.50
hsa-let-7c-5p	274-280	7mer-m8	-0.43	96	-0.43	3.218	0.50
hsa-let-7b-5p	274-280	7mer-m8	-0.43	96	-0.43	3.218	0.50
hsa-let-7e-5p	274-280	7mer-m8	-0.44	96	-0.44	3.218	0.50
hsa-let-7f-5p	274-280	7mer-m8	-0.42	96	-0.42	3.218	0.50
hsa-miR-98-5p	274-280	7mer-m8	-0.42	96	-0.42	3.218	0.50
hsa-miR-4458	274-280	7mer-m8	-0.41	95	-0.41	3.218	0.50
hsa-miR-4500	274-280	7mer-m8	-0.40	95	-0.40	3.218	0.50
hsa-miR-30e-5p	285-292	8mer	-0.54	99	-0.54	6.033	0.94
hsa-miR-30b-5p	285-292	8mer	-0.52	99	-0.52	6.033	0.94
hsa-miR-30d-5p	285-292	8mer	-0.54	99	-0.54	6.033	0.94
hsa-miR-30a-5p	285-292	8mer	-0.54	99	-0.54	6.033	0.94
hsa-miR-30c-5p	285-292	8mer	-0.52	99	-0.52	6.033	0.94
hsa-miR-19b-3p	306-313	8mer	-0.54	99	-0.54	6.027	0.86
hsa-miR-19a-3p	306-313	8mer	-0.54	99	-0.54	6.027	0.86
hsa-miR-331-3p	316-322	7mer-m8	-0.28	97	-0.28	4.070	N/A
hsa-miR-5590-3p	402-408	7mer-m8	-0.33	99	-0.32	5.493	0.54
hsa-miR-142-5p	402-408	7mer-m8	-0.31	99	-0.31	5.493	0.54
Poorly conserved sites					
hsa-miR-4520-5p	19-25	7mer-m8	-0.26	80	-0.26	0.000	N/A
hsa-miR-569	26-32	7mer-m8	-0.06	64	-0.06	0.057	N/A
hsa-miR-324-5p	34-40	7mer-m8	-0.33	94	-0.33	0.051	N/A
hsa-miR-7-2-3p	49-55	7mer-1A	-0.07	96	-0.07	0.000	N/A
hsa-miR-7-1-3p	49-55	7mer-1A	-0.09	96	-0.09	0.000	N/A



	A	B	C	D	E	F	G	H
1	miRNA	Position in t	seed match	context++ s	context++ s	weighted cc	conserved b	Pct
2	Conserved sites							
3	hsa-miR-21	68-74	7mer-m8	-0.17	85	-0.17	6.478	0.85
4	hsa-miR-14	80-87	8mer	-0.13	86	-0.13	3.466	0.6
5	hsa-miR-20	80-87	8mer	-0.13	86	-0.13	3.466	0.6
6	hsa-miR-14	114-120	7mer-1A	-0.07	73	-0.07	4.252	0.29
7	hsa-miR-20	114-120	7mer-1A	-0.07	73	-0.07	4.252	0.29
8	hsa-miR-19	142-148	7mer-m8	-0.19	91	-0.19	5.566	0.59
9	hsa-miR-36	287-293	7mer-m8	-0.29	95	-0.29	8.147	0.92
10	hsa-miR-36	287-293	7mer-m8	-0.29	95	-0.29	8.147	0.92
11	hsa-miR-80	315-321	7mer-1A	-0.08	82	-0.08	4.366	0.45
12	hsa-miR-37	323-329	7mer-1A	-0.11	88	-0.11	6.872	0.35
13	hsa-miR-15	400-406	7mer-m8	-0.14	87	-0.14	4.712	N/A

[Download table]

Conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 24-31 of SOCS1 3' UTR hsa-miR-155-5p	5' ...GCCCGCCGUGCACGC--AGCAUUAA... 3' UGGGGAUAGUGCUAAUCGUAAUU	8mer	-0.33	97	-0.33	3.691	0.38

Gencode transcript ID	ENST00000332029.2
miRBase ID	hsa-miR-155-5p
position of site	24-31
site type	-0.589
supplementary pairing	-0.040
local AU	0.019
min dist	-0.004
sRNA1A	0
sRNA1C	0
sRNA1G	0
sRNA8A	0
sRNA8C	0
sRNA8G	0
site8A	0
site8C	0
site8G	0
UTR length	0.046
SA	-0.001
ORF length	0.005
ORF 8mer count	0
offset 6mer count	0
TA	0.088
SPS	0.193
PCT	-0.049
context++ score	**-0.332**
AIR	**1.000**
weighted context++ score	**-0.332**

اطلاعات
context score

* **SOCS1 (suppressor of cytokine signaling1)**

* **CTLA4(Cytotoxic T-lymphocyte Antigen Protein 4)**

* **TAB2 (TGF-beta activated kinase 1/MAP3K7 binding protein 2)**

* **IKBKE (Inhibitor of nuclear factor kappa-B kinase subunit epsilon)**

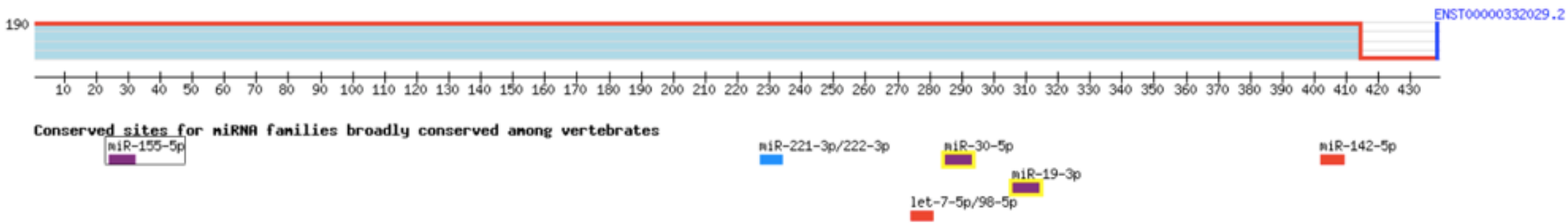
* **MMP16 (matrix metallo peptidase 16)**

* **MYD88 (myeloid differentiation primary response 88)**

SOCS-1 (8)

TargetScanHuman
Prediction of microRNA targets Release 7.1: June 2016 Agarwal *et al.*, 2015

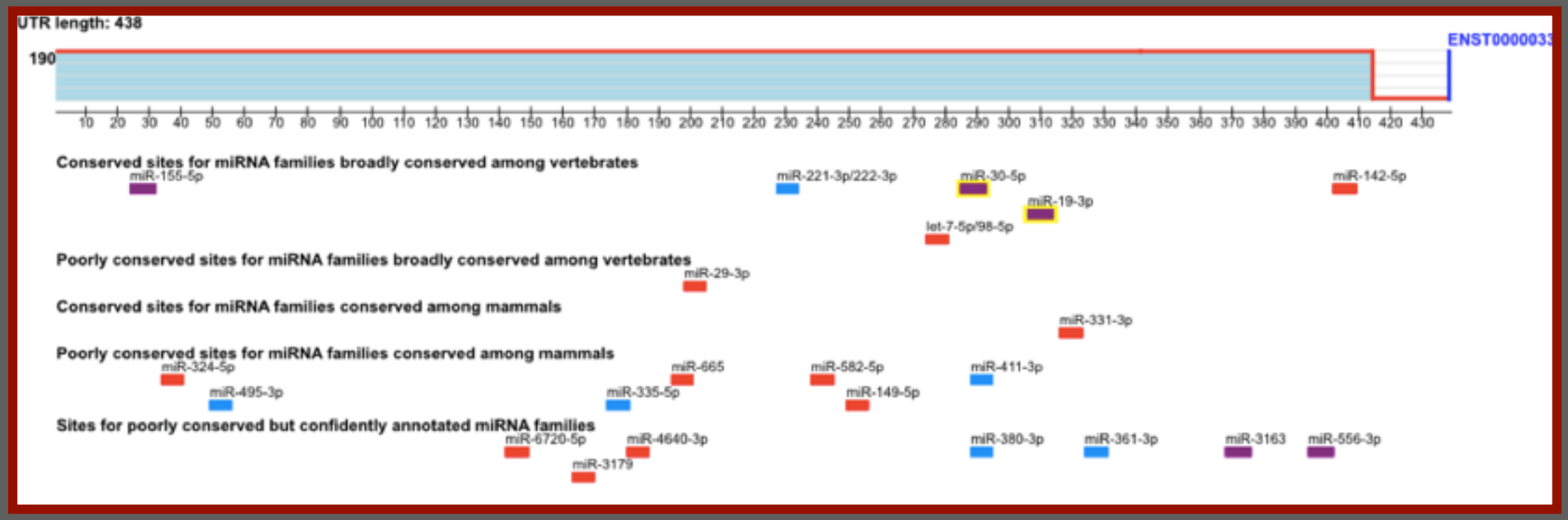
Human SOCS1 ENST00000332029.2 3' UTR length: 438

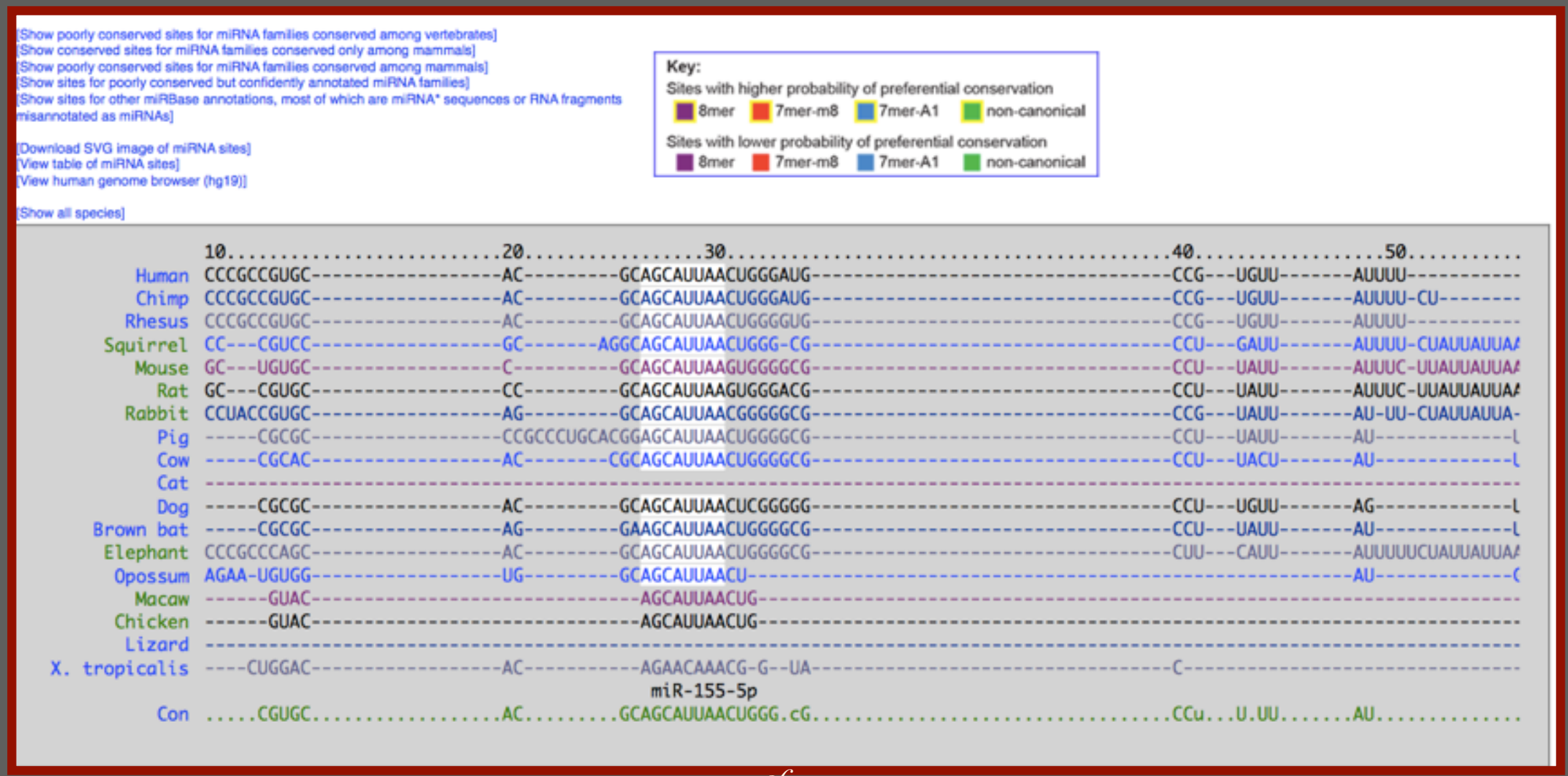


[Show poorly conserved sites for miRNA families conserved among vertebrates]
[Show conserved sites for miRNA families conserved only among mammals]
[Show poorly conserved sites for miRNA families conserved among mammals]
[Show sites for poorly conserved but confidently annotated miRNA families]
[Show sites for other miRBase annotations, most of which are miRNA* sequences or RNA fragments misannotated as miRNAs]

[Download SVG image of miRNA sites]
[View table of miRNA sites]
[View human genome browser (hg19)]

Key:
Sites with higher probability of preferential conservation
8mer 7mer-m8 7mer-A1 non-canonical
Sites with lower probability of preferential conservation
8mer 7mer-m8 7mer-A1 non-canonical


UTR length: 438
190
ENST0000033
10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430
Conserved sites for miRNA families broadly conserved among vertebrates
miR-155-5p
miR-221-3p/222-3p
miR-30-5p
miR-142-5p
miR-19-3p
let-7-5p/98-5p
Poorly conserved sites for miRNA families broadly conserved among vertebrates
miR-29-3p
Conserved sites for miRNA families conserved among mammals
miR-331-3p
Poorly conserved sites for miRNA families conserved among mammals
miR-324-5p
miR-665
miR-582-5p
miR-411-3p
miR-495-3p
miR-335-5p
miR-149-5p
Sites for poorly conserved but confidently annotated miRNA families
miR-6720-5p
miR-4640-3p
miR-380-3p
miR-361-3p
miR-3163
miR-556-3p
miR-3179


[Show poorly conserved sites for miRNA families conserved among vertebrates]
[Show conserved sites for miRNA families conserved only among mammals]
[Show poorly conserved sites for miRNA families conserved among mammals]
[Show sites for poorly conserved but confidently annotated miRNA families]
[Show sites for other miRBase annotations, most of which are miRNA* sequences or RNA fragments misannotated as miRNAs]
[Download SVG image of miRNA sites]
[View table of miRNA sites]
[View human genome browser (hg19)]
[Show all species]
Key:
Sites with higher probability of preferential conservation
8mer 7mer-m8 7mer-A1 non-canonical
Sites with lower probability of preferential conservation
8mer 7mer-m8 7mer-A1 non-canonical
10.....20.....30.....40.....50.....
Human CCCGCCGUGC----------AC---------GCAGCAUUAACUGGGAUG----------CCG---UGUU-------AUUUU----------
Chimp CCCGCCGUGC----------AC---------GCAGCAUUAACUGGGAUG----------CCG---UGUU-------AUUUU-CU--------
Rhesus CCCGCCGUGC----------AC---------GCAGCAUUAACUGGGGUG----------CCG---UGUU-------AUUUU----------
Squirrel CC---CGUCC----------GC-------AGGCAGCAUUAACUGGG-CG----------CCU---GAUU-------AUUUU-CUAUUAUUAA
Mouse GC---UGUGC----------C----------GCAGCAUUAAGUGGGGCG----------CCU---UAUU-------AUUUC-UUAUUAUUAA
Rat GC---CGUGC----------CC---------GCAGCAUUAAGUGGGACG----------CCU---UAUU-------AUUUC-UUAUUAUUAA
Rabbit CCUACCGUGC----------AG---------GCAGCAUUAACGGGGGCG----------CCG---UAUU-------AU-UU-CUAUUAUUA-
Pig -----CGCGC----------CCGCCCUGCACGGAGCAUUAACUGGGGCG----------CCU---UAUU-------AU----------L
Cow -----CGCAC----------AC--------CGCAGCAUUAACUGGGGCG----------CCU---UACU-------AU----------L
Cat ----------
Dog -----CGCGC----------AC---------GCAGCAUUAACUCGGGGG----------CCU---UGUU-------AG----------L
Brown bat -----CGCGC----------AG---------GAAGCAUUAACUGGGGCG----------CCU---UAUU-------AU----------L
Elephant CCCGCCCAGC----------AC---------GCAGCAUUAACUGGGGCG----------CUU---CAUU-------AUUUUUCUAUUAUUAA
Opossum AGAA-UGUGG----------UG---------GCAGCAUUAACU----------AU----------C
Macaw ------GUAC----------AGCAUUAACUG----------
Chicken ------GUAC----------AGCAUUAACUG----------
Lizard ----------
X. tropicalis ----CUGGAC----------AC----------AGAACAAACG-G--UA----------C----------
miR-155-5p
Con .....CGUGC.....AC.....GCAGCAUUAACUGGG.cG.....CCu...U.UU.....AU.....

[Download table]

Conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 24-31 of SOCS1 3' UTR	5' ...GCCCGCCGUGCACGC--AGCAUUAA...	8mer	-0.33	97	-0.33	3.691	0.38
hsa-miR-155-5p	3' UGGGGAUAGUGCUAAUCGUAAUU						

Context++ score and features that contribute to the context++ score are evaluated as in Agarwal et al., 2015.
Conserved branch lengths and P_{CT} are evaluated as in Friedman et al., 2008, with an expanded 84-species alignment as described in Agarwal et al., 2015.

Poorly conserved

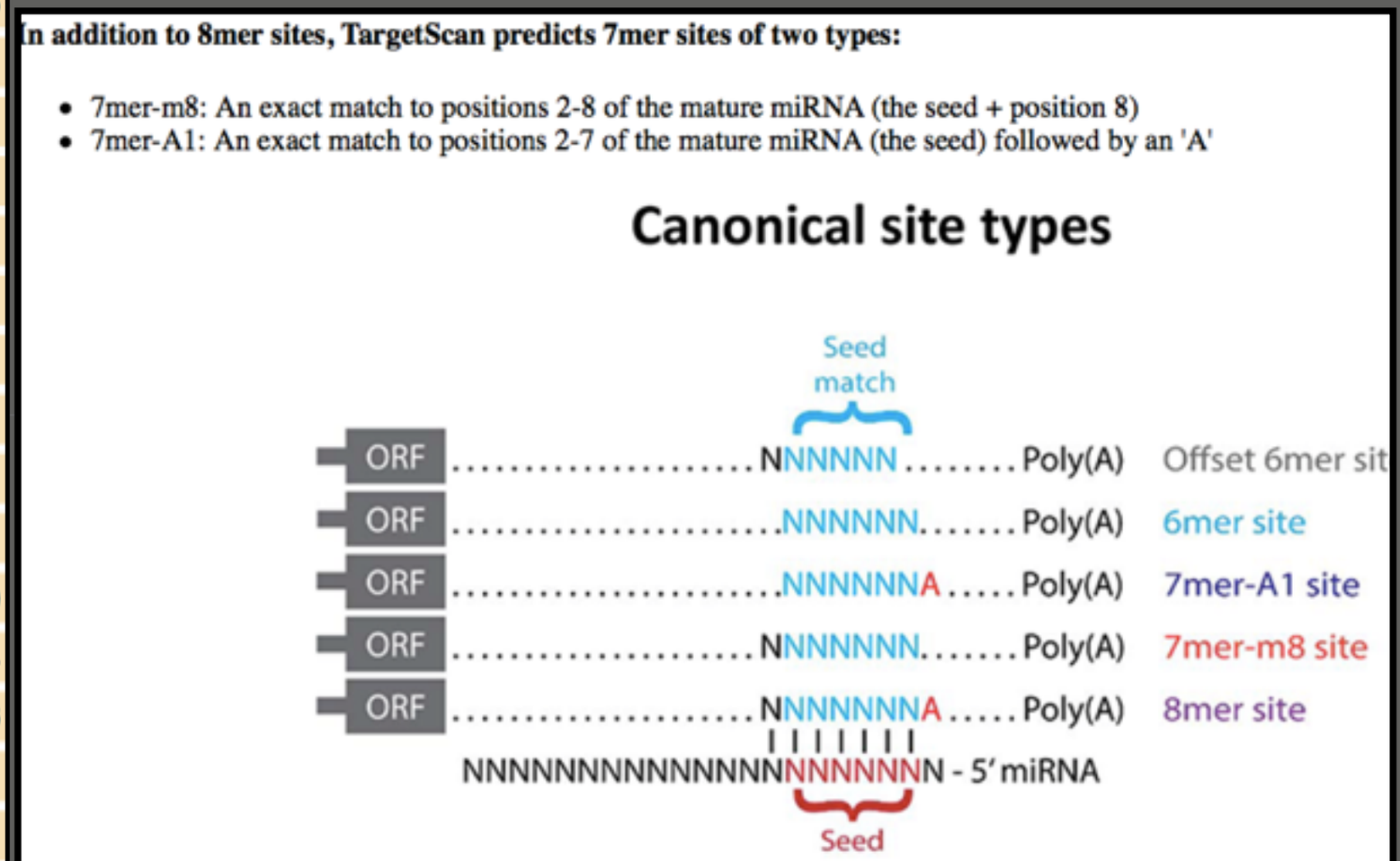
Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}

Context++ score and features that contribute to the context++ score are evaluated as in Agarwal et al., 2015.
Conserved branch lengths and P_{CT} are evaluated as in Friedman et al., 2008, with an expanded 84-species alignment as described in Agarwal et al., 2015.

Gencode transcript ID	ENST00000306503.5
miRBase ID	hsa-miR-155-5p
position of site	2062-2068
site type	-0.224
supplementary pairing	-0.022
local AU	-0.169
min dist	0.045
sRNA1A	0
sRNA1C	0
sRNA1G	0
sRNA8A	0
sRNA8C	0
sRNA8G	0
site8A	0
site8C	0
site8G	0
UTR length	0.130
SA	-0.124
ORF length	0.046
ORF 8mer count	0
offset 6mer count	0
TA	0.058
SPS	0.123
PCT	-0.031
context++ score	**-0.168**
AIR	**1.000**
weighted context++ score	**-0.168**

In addition to 8mer sites, TargetScan predicts 7mer sites of two types:

- 7mer-m8: An exact match to positions 2-8 of the mature miRNA (the seed + position 8)
- 7mer-A1: An exact match to positions 2-7 of the mature miRNA (the seed) followed by an 'A'



CTLA4(9)

This gene is a member of the **immunoglobulin** superfamily
and encodes a protein which
transmits an inhibitory signal to T cells
Mutations in this gene autoimmune diseases

[Download table]

Conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 296-302 of CTLA4 3' UTR	5' ...UUAAUAUGGGGAUGCAGCAUUAU...	7mer-m8	-0.22	90	-0.22	3.270	0.23
hsa-miR-155-5p	3' UGGGGAUAGUGCUAAUCGUAAUU						

Context++ score and features that contribute to the context++ score are evaluated as in Agarwal et al., 2015.
Conserved branch lengths and P_{CT} are evaluated as in Friedman et al., 2008, with an expanded 84-species alignment as described in Agarwal et al., 2015.

TAB2 (10)

regulate the development and function of osteoclasts

Conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 818-825 of TAB2 3' UTR	5' ...GCCUUAAAAUAAAAAAGCAUUAA...	8mer	-0.30	95	-0.30	4.173	0.49
hsa-miR-155-5p	3' UGGGGAUAGUGCUAAUCGUAAUU						

Context++ score and features that contribute to the context++ score are evaluated as in Agarwal et al., 2015.

Conserved branch lengths and P_{CT} are evaluated as in Friedman et al., 2008, with an expanded 84-species alignment as described in Agarwal et al., 2015.

Poorly conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 1956-1963 of TAB2 3' UTR	5' ...UCAGCAGAUCAUUUA-AGCAUUAA...	8mer	-0.26	93	0.00	0.683	< 0.1
hsa-miR-155-5p	3' UGGGGAUAGUGCUAAUCGUAAUU						

MicroRNA-155 modulates the interleukin-1 signaling pathway in activated human monocyte-derived dendritic cells

IKBKE (11)

Inhibitor of nuclear factor kappa-B kinase subunit epsilon

	Predicted consequential pairing of target region (top) and miRNA (bottom)		Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 29-35 of IKBKE 3' UTR	5'	...CAUGAGGCAUCCUGAAGCAUUAG...	7mer-m8	-0.17	85	-0.17	4.392	0.23
hsa-miR-155-5p	3'	UGGGGAUAGUGCUAAUCGUAAUU						
Position 107-113 of IKBKE 3' UTR	5'	...UCCCAUCACAUCAGCCUACCUCC...	7mer-m8	-0.35	93	-0.35	4.780	0.89
hsa-let-7b-5p	3'	UUGGUGUGUUGGAUGAUGGAGU						
Position 107-113 of IKBKE 3' UTR	5'	...UCCCAUCACAUCAGCCUACCUCC...	7mer-m8	-0.35	93	-0.35	4.780	0.89
hsa-let-7i-5p	3'	UUGUCGUGUUUGAUGAUGGAGU						
Position 107-113 of IKBKE 3' UTR	5'	...UCCCAUCACAUCAGCCUACCUCC...	7mer-m8	-0.34	92	-0.34	4.780	0.89

MMP16

Download table]

Conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 3055-3062 of MMP16 3' UTR	5' ...CUAGAAAAUAAUCAUAGCAUUAA...	8mer	-0.07	60	-0.07	2.343	< 0.1
hsa-miR-155-5p	3' UGGGGAUAGUGCUAAUCGUAAUU						

Context++ score and features that contribute to the context++ score are evaluated as in Agarwal et al., 2015.
Conserved branch lengths and P_{CT} are evaluated as in Friedman et al., 2008, with an expanded 84-species alignment as described in Agarwal et al., 2015.

Poorly conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 3907-3913 of MMP16 3' UTR	5' ...AGAGCUAAAUUAGACAGCAUUAU...	7mer-m8	-0.03	35	-0.03	0.117	< 0.1
hsa-miR-155-5p	3' UGGGGAUAGUGCUAAUCGUAAUU						

Context++ score and features that contribute to the context++ score are evaluated as in Agarwal et al., 2015.
Conserved branch lengths and P_{CT} are evaluated as in Friedman et al., 2008, with an expanded 84-species alignment as described in Agarwal et al., 2015.

tics and Research Computing
16 Whitehead Institute for Biomedical Research

TargetScan Release 7.1
Questions: wibr-bioinformatics@wi.mit.edu

MYD88(12)

Conserved

Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}

Context++ score and features that contribute to the context++ score are evaluated as in Agarwal et al., 2015.
Conserved branch lengths and P_{CT} are evaluated as in Friedman et al., 2008, with an expanded 84-species alignment as described in Agarwal et al., 2015.

Poorly conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 77-83 of MYD88 3' UTR hsa-miR-155-3p	5' ...GCCUCCUCCUUUCGUUGUAGGAG... 3' ACAAUUACGAUUAUACAUCCUC	7mer-m8	-0.03	26	-0.03	0	N/A
Position 368-375 of MYD88 3' UTR hsa-miR-155-3p	5' ...CUGUGUUUGAAUCCCUGUAGGAA... 3' ACAAUUACGAUUAUACAUCCUC	8mer	-0.24	89	-0.24	0	N/A

Results

- Since **miRNAs** are involved in a variety of **biological processes** and their **deregulation** can be linked to **cancer** and several **other diseases**, they have a **huge impact on biomedical research.**
- Despite the large number of studies carried out to date, our **understanding of miRNAs** and their **large scale regulatory mechanisms** is still **limited**

now **bioinformatic tools** are making it possible to address all the aspects of miRNA research pipelines.

Results

*The most common and vital **limitation** of these computational tools is generation of large amounts of **false-positive** data.

Since **miRNAs are frequently dysregulated in human disease**, they are considered as **promising targets for therapeutic intervention**. A **powerful bioinformatic** platform could play a **crucial role in this type of research** (13).

Results

miR-155 may its inflammation role be more than its protective effect in patients with rheumatoid arthritis .

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